## AMENDMENTS TO THE SPECIFICATION

Please replace the two paragraphs on page 20, line 12 to page 21, line 10 with the following amended paragraphs:

Other exemplary oncogenes are well known in the art and several such examples are described in, for example, *The Genetic Basis of Human Cancer* (Vogelstein, B. and Kinzler, K.W. eds.. McGraw-Hill, New York, NY, 1998), such as in Tables 5.1-5.3 of Look, A.T., *Genes altered by chromosomal translocations in leukemias and lymphoma*, pages 109-141, which is incorporated herein by reference in its entirety. Mammalian homologues of such genes are preferred because they can be distinguished from endogenous fish genes. Further preferred are human homologues of such genes. The corresponding sequences of such oncogenes, including the human homologues of the oncogenes, are known and may be found, for example, in the NCBI database ~~(www.ncbi.nlm.nih.gov)~~.

The oncogene is selected based on the form of cancer it is desired that the transgenic fish will develop. For example, mutated or activated genes of the *RAS* family may be used for induction of a wide variety of types of cancers, such as renal, pancreatic or colon cancers, and *HOX11* and *TAL1* may be used for T-cell cancer induction, *etc.* Preferably the oncogenes are T-cell or B-cell oncogenes. Most preferably, the T-cell oncogenes are members of the *MYC*, T*AL1/SCL, TAL2, LYL1, LMO1, LMO2, HOX11, TAN1,* and *LYL1* gene families, and the B-cell oncogenes are members of the *MYC, E2A-PBX1, E2A-HLF, TEL-AML1, BCL6, BCL3, LYT10, MLL, HOX* or *PAX5* gene families. In one form, the oncogene is *MYC*, such as *c-MYC* (GenBank Accession No. XM_122917.1~~, available at http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Nucleotide~~). Expression of such a nucleotide sequence in T-cell progenitors of the fish leads to development of acute T-cell lymphoblastic leukemia or lymphoma. The invention is not limited to such an oncogene sequence. For example, altered forms of the oncogene nucleotide sequence, such as *cMYC* or the other oncogene nucleotide sequences described herein, that increase or decrease the transformation potential of the oncogene are also envisioned.

Please replace the paragraph at page 21, line 16 to 23 with the following amended paragraph:

Percent identity may be determined, for example, by comparing sequence information using the advanced BLAST computer program, version 2.0.8, available from the National Institutes of Health ~~(www.ncbi.nlm.nih.gov/BLAST)~~. The BLAST program is based on the alignment method of Karlin and Altschul, (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268 and as discussed in Altschul, *et al.*, (1990) *J. Mol. Biol.* 215:403-410; Karlin and Altschul, *Proc. Natl. Acad. Sci. USA* (1993) 90:5873-5877; and Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402.